4 pgs · SEQ. List

Table 6

CD28TFc sequence (SEQ ID NO:2)

(thrombin site separating the two halves of the chimera is shown in bold)


```
        CCCCATCCGCTCAAGCAGGCCACCATGGATTGGCTGCGGAACTTGCTATTCCTGATGGCG
   1    ---------+---------+---------+---------+---------+---------+  60
        GGGGTAGGCGAGTTCGTCCGGTGGTACCTAACCGACGCCTTGAACGATAAGGACTACCGC

   a                              M  D  W  L  R  N  L  L  F  L  M  A  -


        GCCGCTCAAAGTATCAACGCGAACAAGATCTTGGTGAAGCAGTCGCCCATGCTTGTAGCG
  61    ---------+---------+---------+---------+---------+---------+ 120
        CGGCGAGTTTCATAGTTGCGCTTGTTCTAGAACCACTTCGTCAGCGGGTACGAACATCGC

   a    A  A  Q  S  I  N  A  N  K  I  L  V  K  Q  S  P  M  L  V  A  -


        TACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTTCTCAAGGGAGTTC
 121    ---------+---------+---------+---------+---------+---------+ 180
        ATGCTGTTACGCCAGTTGGAATCGACGTTCATAAGGATGTTAGAGAAGAGTTCCCTCAAG

   a    Y  D  N  A  V  N  L  S  C  K  Y  S  Y  N  L  F  S  R  E  F  -


        CGGGCATCCCTTCACAAAGGACTGGATAGTGCTGTGGAAGTCTGTGTTGTATATGGGAAT
 181    ---------+---------+---------+---------+---------+---------+ 240
        GCCCGTAGGGAAGTGTTTCCTGACCTATCACGACACCTTCAGACACAACATATACCCTTA

   a    R  A  S  L  H  K  G  L  D  S  A  V  E  V  C  V  V  Y  G  N  -


        TACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTTCAACTGTGATGGGAAATTGGGC
 241    ---------+---------+---------+---------+---------+---------+ 300
        ATGAGGGTCGTCGAAGTCCAAATGAGTTTTTGCCCCAAGTTGACACTACCCTTTAACCCG

   a    Y  S  Q  Q  L  Q  V  Y  S  K  T  G  F  N  C  D  G  K  L  G  -


        AATGAATCAGTGACATTCTACCTCCAGAATTTGTATGTTAACCAAACAGATATTTACTTC
 301    ---------+---------+---------+---------+---------+---------+ 360
        TTACTTAGTCACTGTAAGATGGAGGTCTTAAACATACAATTGGTTTGTCTATAAATGAAG

   a    N  E  S  V  T  F  Y  L  Q  N  L  Y  V  N  Q  T  D  I  Y  F  -
```

118

```
       TGCAAAATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAGAGCAATGGTACC
361    ---------+---------+---------+---------+---------+---------+  420
       ACGTTTTAACTTCAATACATAGGAGGAGGAATGGATCTGTTACTCTTCTCGTTACCATGG

a         C  K  I  E  V  M  Y  P  P  P  Y  L  D  N  E  K  S  N  G  T   -


       ATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGTCCGCTATTTCCCGGACCTTCTAAG
421    ---------+---------+---------+---------+---------+---------+  480
       TAATAGGTACACTTTCCCTTTGTGGAAACAGGTTCAGGCGATAAAGGGCCTGGAAGATTC

a         I  I  H  V  K  G  K  H  L  C  P  S  P  L  F  P  G  P  S  K   -


       CCCCTGGTACCCAGGGGTAGTGGTAGTAAGCCTAGCATAAGTACAGTCCCAGAAGTATCA
481    ---------+---------+---------+---------+---------+---------+  540
       GGGGACCATGGGTCCCCATCACCATCATTCGGATCGTATTCATGTCAGGGTCTTCATAGT

a         P  L  V  P  R  G  S  G  S  K  P  S  I  S  T  V  P  E  V  S   -


       TCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAG
541    ---------+---------+---------+---------+---------+---------+  600
       AGACAGAAGTAGAAGGGGGGTTTCGGGTTCCTACACGAGTGGTAATGAGACTGAGGATTC

a         S  V  F  I  F  P  P  K  P  K  D  V  L  T  I  T  L  T  P  K   -


       GTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTT
601    ---------+---------+---------+---------+---------+---------+  660
       CAGTGCACACAACACCATCTGTAGTCGTTCCTACTAGGGCTCCAGGTCAAGTCGACCAAA

a         V  T  C  V  V  V  D  I  S  K  D  D  P  E  V  Q  F  S  W  F   -


       GTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGC
661    ---------+---------+---------+---------+---------+---------+  720
       CATCTACTACACCTCCACGTGTGTCGAGTCTGCGTTGGGGCCCTCCTCGTCAAGTTGTCG

a         V  D  D  V  E  V  H  T  A  Q  T  Q  P  R  E  E  Q  F  N  S   -
```

```
      ACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAG
 721  ---------+---------+---------+---------+---------+---------+ 780
      TGAAAGGCGAGTCAGTCACTTGAAGGGTAGTACGTGGTCCTGACCGAGTTACCGTTCCTC

  a    T  F  R  S  V  S  E  L  P  I  M  H  Q  D  W  L  N  G  K  E   -
```

```
      TTCAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAACCATCTCCAAA
 781  ---------+---------+---------+---------+---------+---------+ 840
      AAGTTTACGTCCCAGTTGTCACGTCGAAAGGGACGGGGGTAGCTCTTTTGGTAGAGGTTT

  a    F  K  C  R  V  N  S  A  A  F  P  A  P  I  E  K  T  I  S  K   -
```

```
      ACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATG
 841  ---------+---------+---------+---------+---------+---------+ 900
      TGGTTTCCGTCTGGCTTCCGAGGTGTCCACATGTGGTAAGGTGGAGGGTTCCTCGTCTAC

  a    T  K  G  R  P  K  A  P  Q  V  Y  T  I  P  P  P  K  E  Q  M   -
```

```
      GCCAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACT
 901  ---------+---------+---------+---------+---------+---------+ 960
      CGGTTCCTATTTCAGTCAGACTGGACGTACTATTGTCTGAAGAAGGGACTTCTGTAATGA

  a    A  K  D  K  V  S  L  T  C  M  I  T  D  F  F  P  E  D  I  T   -
```

```
      GTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATG
 961  ---------+---------+---------+---------+---------+---------+ 1020
      CACCTCACCGTCACCTTACCCGTCGGTCGCCTCTTGATGTTCTTGTGAGTCGGGTAGTAC

  a    V  E  W  Q  W  N  G  Q  P  A  E  N  Y  K  N  T  Q  P  I  M   -,
```

```
      GACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAG
1021  ---------+---------+---------+---------+---------+---------+ 1080
      CTGTGTCTACCGAGAATGAAGCAGATGTCGTTCGAGTTACACGTCTTCTCGTTGACCCTC

  a    D  T  D  G  S  Y  F  V  Y  S  K  L  N  V  Q  K  S  N  W  E   -
```

120

```
      GCAGGAAATACTTTCACCTGCTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAG
1081  ---------+---------+---------+---------+---------+---------+ 1140
      CGTCCTTTATGAAAGTGGACGAGACACAATGTACTCCCGGACGTGTTGGTGGTATGACTC

a     A  G  N  T  F  T  C  S  V  L  H  E  G  L  H  N  H  H  T  E  -
```

```
      AAGAGCCTCTCCCACTCTCCTGGTAAATAA
1141  ---------+---------+---------+ 1170
      TTCTCGGAGAGGGTGAGAGGACCATTTATT

a     K  S  L  S  H  S  P  G  K  *  -
```